Figure 1: Full-length Sequence of C. pneumoniae 76kDa Gene.

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ataa	ıtaaa	aac t	aaaa	igatt	it tt	atta	tttt	ttg	gagtt	ttt				cct Pro		115.
ggt Gly	cca Pro	ggt Gly	cct Pro	ata Ile 10	gac Asp	gaa Glu	aca Thr	gaa Glu	cgc Arg 15	aca Thr	cct Pro	ccc Pro	gca Ala	gat Asp 20	ctt Leu	163
tct Ser	gct Ala	caa Gln	gga Gly 25	ttg Leu	gag Glu	gcg Ala	agt Ser	gca Ala 30	gca Ala	aat Asn	aag Lys	agt Ser	gcg Ala 35	gaa Glu	gct Ala	211
caa Gln	aga Arg	ata Ile 40	gca Ala	ggt Gly	gcg Ala	gaa Glu	gct Ala 45	aag Lys	cct Pro	aaa Lys	gaa Glu	tct Ser 50	aag Lys	acc Thr	gat Asp	259
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agt Ser 70	ctg Leu	gca Ala	gat Asp	aag Lys	ctg Leu 75	ggt Gly	att Ile	gct Ala	tct Ser	agt Ser 80	aac Asn	agc Ser	tcg Ser	tct Ser	tct Ser 85	355
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cct Pro	cct Pro	cca Pro	ccc Pro 105	acg Thr	ttt Phe	gat Asp	gat Asp	tat Tyr 110	aag Lys	act Thr	caa Gln	gcg Ala	caa Gln 115	aca Thr	gct Ala	451
tac Tyr	gat Asp	act Thr 120	atc Ile	ttt Phe	acc Thr	tca Ser	aca Thr 125	tca Ser	cta Leu	gct Ala	gac Asp	ata Ile 130	cag Gln	gct Ala	gct Ala	499
ttg Leu	gtg Val 135	agc Ser	ctc Leu	cag Gln	gat Asp	gct Ala 140	gtc Val	act Thr	aat Asn	ata Ile	aag Lys 145	gat Asp	aca Thr	gcg Ala	gct Ala	547
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gat Asp	gca Ala	gtt Val	aaa Lys	gtt Val 170	ggc Gly	gcg Ala	caa Gln	att Ile	aca Thr 175	gaa Glu	tta Leu	gcg Ala	aaa Lys	tat Tyr 180	gct Ala	643
tcg Ser	gat Asp	aac Asn	caa Gln 185	gcg Ala	att Ile	ctt Leu	gac Asp	tct Ser 190	tta Leu	ggt Gly	aaa Lys	ctg Leu	act Thr 195	tcc Ser	ttc Phe	691

Figure 1 (continued)

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		_			-		_	-			gct Ala					931
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			-			_		-			gac Asp 305					1027
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Figure 1 (continued)

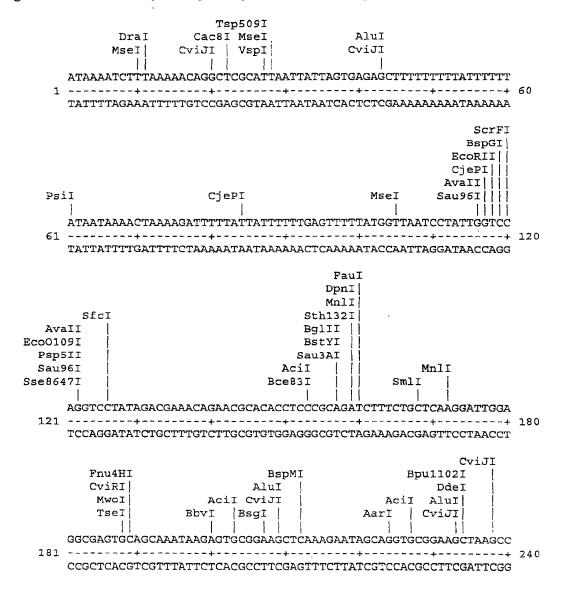
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			Thr					Phe			cct Pro		Val			1891
tct			585					590					595			
		-	tct		_	_		ata	_		tta Leu	~	agt	_		1939
Ser gct	Asn gaa	Asp 600 gga	tct Ser	Thr	Gln	Lys gca	Phe 605 gct	ata Ile gaa	Ala	Lys aaa		Glu 610 ctt	agt Ser	Leu	Phe gaa	1939 1987

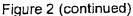
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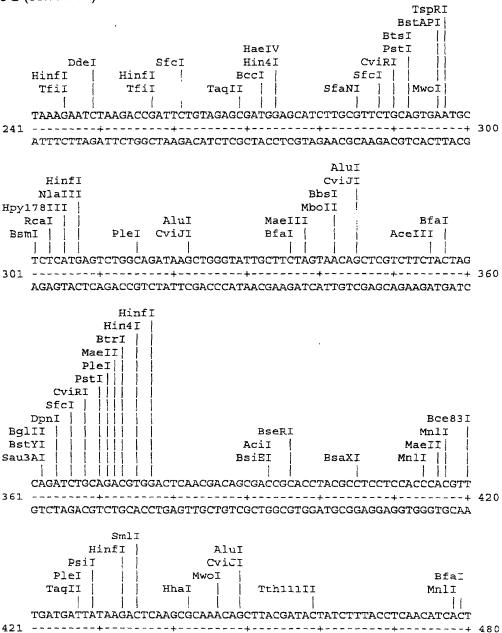
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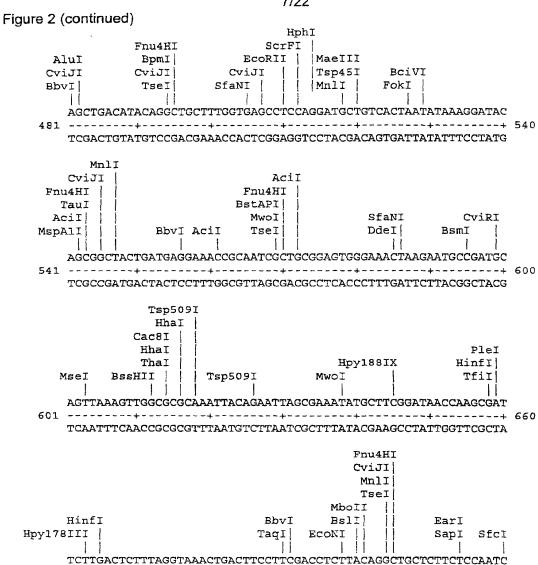
Figure 2: Restriction enzyme map of C. pneumoniae 76kDa gene.







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Figure 2 (continued)

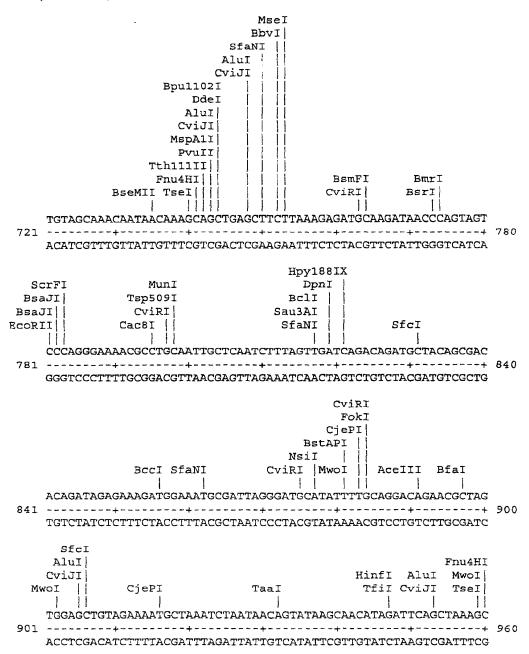


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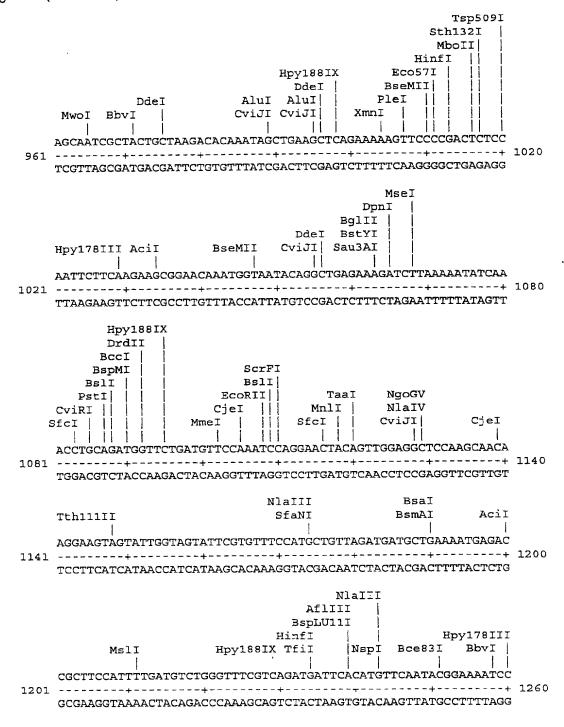
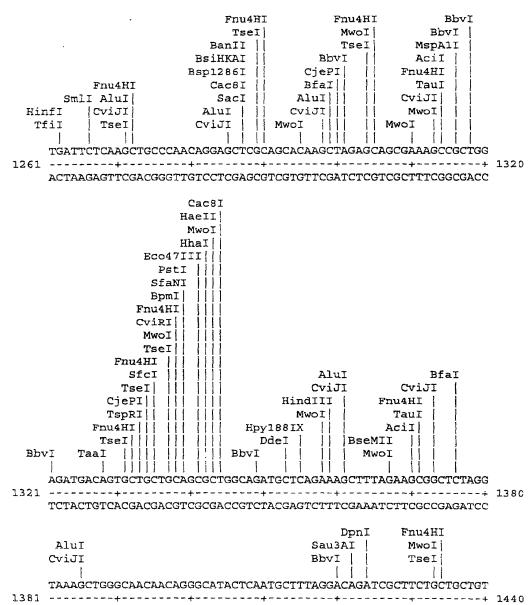


Figure 2 (continued)



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Figure 2 (continued)

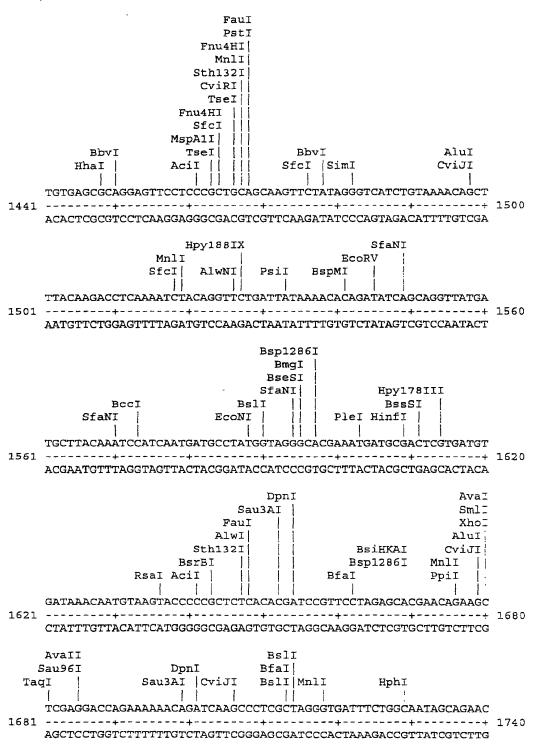


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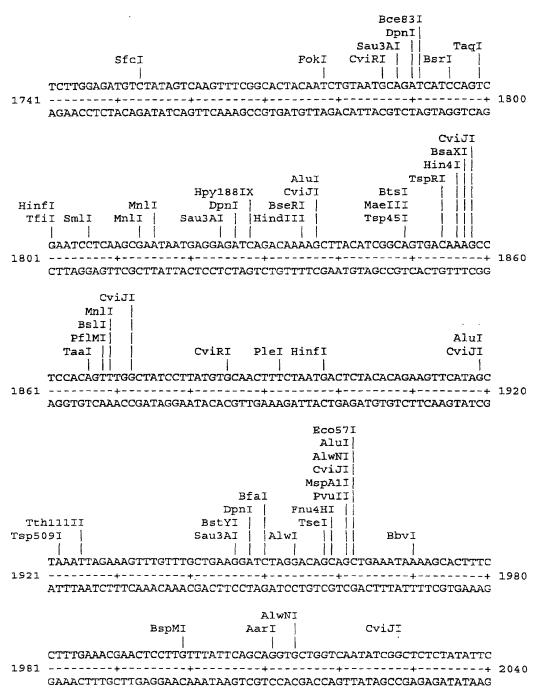


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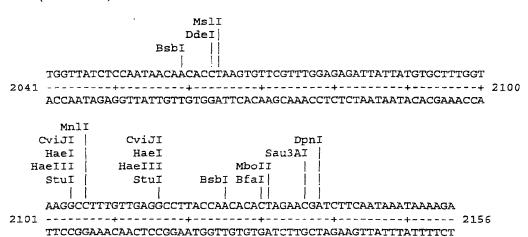


Figure 3: Sequence Containing Truncated Version of *C. pneumoniae* 76kDa Gene; (nucleotides 1 to 665 and 2122 to 2238 are unrelated to the 76kDa Gene).

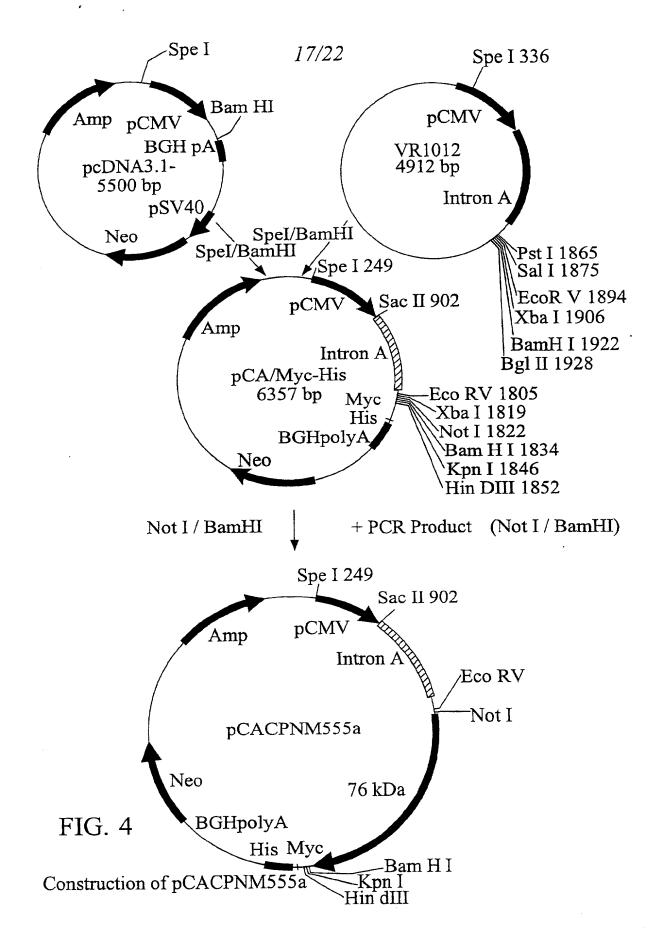
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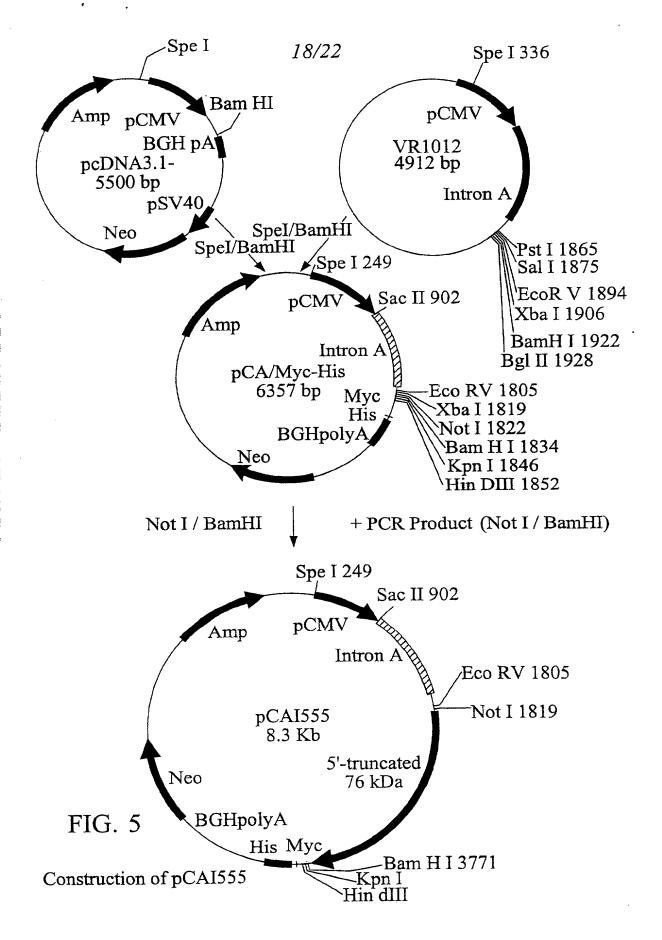
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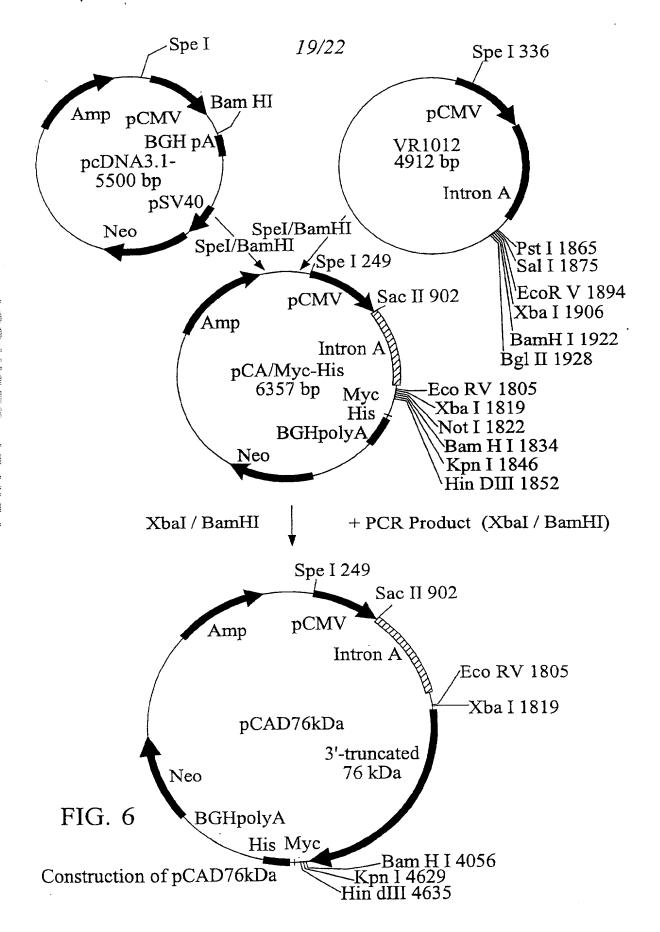
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Figure 3 (continued)

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20/22



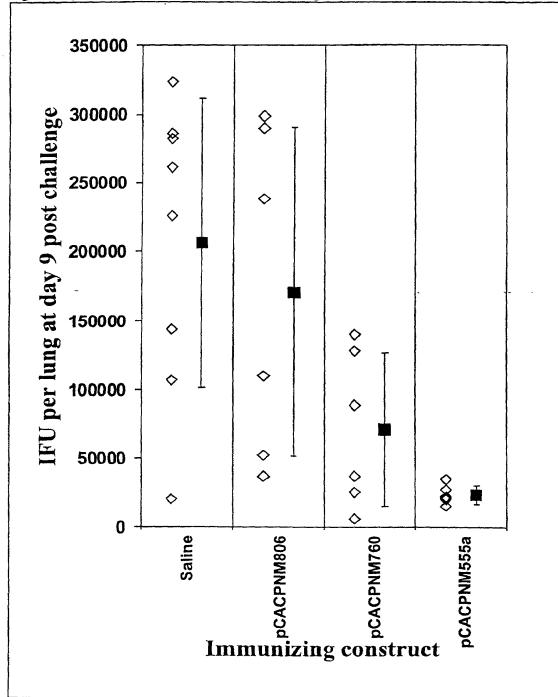


Figure 8: pCAI555 Confers Protection Against C. pneumoniae Infection.

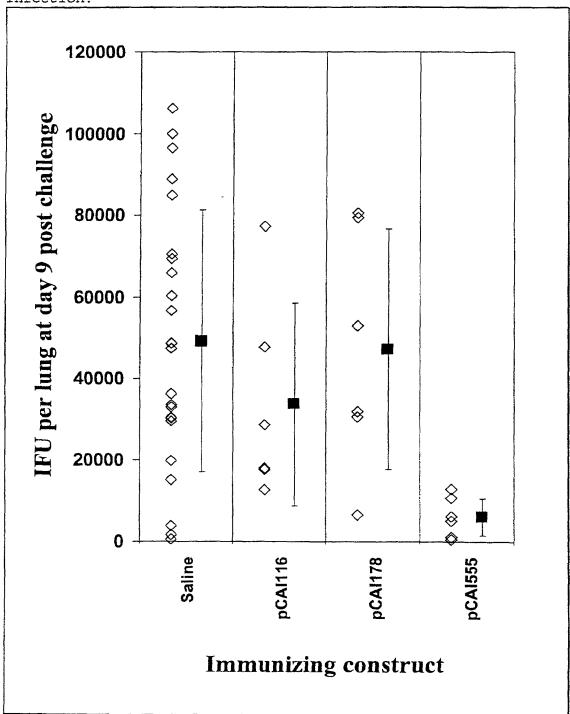
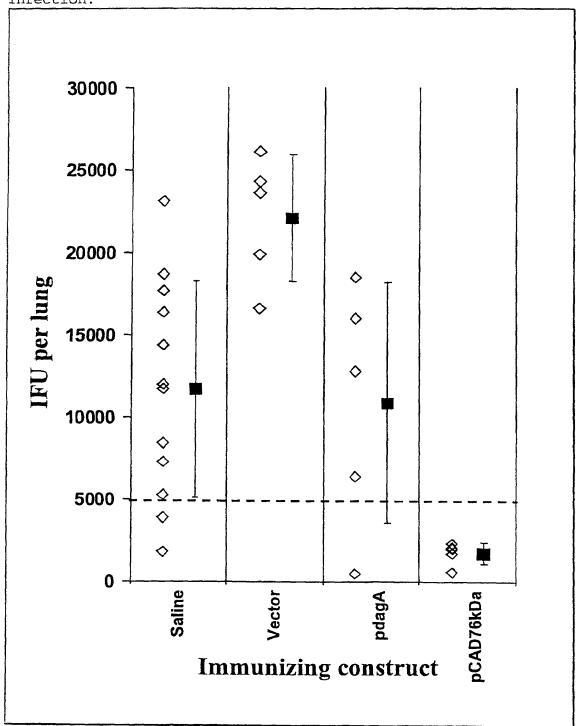


Figure 9: pCAD76kDa Confers Protection against C. pneumoniae Infection.



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- Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn 325 330 335
- Pro Gly Thr Thr Val Gly Gly Ser Lys Gin Gln Gly Ser Ser Ile Gly 340 345

- Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala 355 360 365
- Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr 370 375 380
- Glu Asn Pro Asp Ser Gln Ala Ala Gln Glu Leu Ala Ala Gln Ala 385 390 395 400
- Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
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- Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln 420 425 430
- Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
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- Ser Ala Gly Val Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val 450 460
- Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr 465 470 475 480
- Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr 485 490 495
- Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser 500 505 510
- Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg
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- Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn 530 540
- Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser 545 550 555
- Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile 565 570 575
- Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr 580 585 590
- Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys 595 600 605
- Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys 610 620
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ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala

165

170

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		_		gaa Glu 250		_	_			_	-					768
				gca Ala					-							816
-				aag Lys				_	_		~ ~	_				-864
	_	_		gat Asp	_	_	_				_			-	_	912
Ser	Met 295 ggg	Leu	Leu cgt	_	Asp	Ala 300 att	Glu	Asn atg	Glu	Thr aat	Ala 305 acg	Ser gaa	Ile aat	Leu	Met	912 960
tct ser 310	Met 295 ggg Gly caa	Leu ttt Phe gct	Leu cgt Arg	Asp cag Gln	Asp atg Met 315 cag	Ala 300 att Ile	Glu cac His	Asn atg Met	Glu ttc Phe gca	Thr aat Asn 320 caa	Ala 305 acg Thr	Ser gaa Glu aga	Ile aat Asn gca	Leu cct Pro	Met gat Asp 325 aaa	
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tct Ser 310 tct Ser gcc Ala	Met 295 ggg Gly caa Gln gct Ala	ttt Phe gct Ala gga Gly	cgt Arg gcc Ala gat Asp 345	Cag Gln Caa Gln 330 gac Asp	Asp atg Met 315 cag Gln agt Ser	Ala 300 att Ile gag Glu gct Ala	Glu cac His ctc Leu gct Ala	Asn atg Met gca Ala gca Ala 350 gct	ttc Phe gca Ala 335 gcg Ala	Thr aat Asn 320 caa Gln ctg Leu caa	Ala 305 acg Thr gct Ala gca Ala	gaa Glu aga Arg gat Asp	aat Asn gca Ala gct Ala 355	cct Pro gcg Ala 340 cag Gln	met gat Asp 325 aaa Lys aaa Lys	960 1008 1056
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Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala 50 60

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Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn
85 90 95

Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr 100 105 110

Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser 115 120 125

Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn 130 140

Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro 145 150 155 160

Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala 165 170 175

Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr 180 185 190

Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn 195 200 205

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- Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val 370 375 380
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- Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu
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- Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln
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- Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu 530 540

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			aac age teg tet Asn Ser Ser Ser	
			gcg acc gca cct Ala Thr Ala Pro 100	_
		_	caa gcg caa aca Gln Ala Gln Thr 115	-

tac Tyr	gat Asp	act Thr 120	atc Ile	ttt Phe	acc Thr	tca Ser	aca Thr 125	tca Ser	cta Leu	gct Ala	gac Asp	ata Ile 130	cag Gln	gct Ala	gct Ala	499
_	-	_		_	-	-	gtc Val				-					547
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	_						gac Asp					_				691
							ctc Leu 205									739
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	_						_						ata Ile 435			1411
gct Ala	tta Leu	gga Gly 440	cag Gln	atc Ile	gct Ala	tct Ser	gct Ala 445	gct Ala	gtt Val	gtg Val	agc Ser	gca Ala 450	gga Gly	gta Val		1456
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110

105

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Lys 145	Asp	Thr	Ala	Ala	Thr 150	Asp	Glu	Glu	Thr	Ala 155	Ile	Ala	Ala	Glu	Trp 160
Glu	Thr	Lys	Asn	Ala 165	Asp	Ala	Val	Lys	Val 170	Gly	Ala	Gln	Ile	Thr 175	Glu
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Lys	Leu	Thr 195	Ser	Phe	Asp	Leu	Leu 200	Gln	Ala	Ala	Leu	Leu 205	Gln	Ser	Val
Ala	Asn 210	Asn	Asn	Lys	Ala	Ala 215	Glu	Leu	Leu	Lys	Glu 220	Met	Gln	Asp	Asn
Pro 225	Val	Val	Pro	Gly	Lys 230	Thr	Pro	Ala	Ile	Ala 235	Gln	Ser	Leu	Val	Asp 240
Gln	Thr	Asp	Ala	Thr 245	Ala	Thr	Gln	Ile	Glu 250	Lys	Asp	Gly	Asn	Ala 255	Ile
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<220>

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Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp

5 10 20

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- Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn 260 265 270
- Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala 275 280 285
- Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro 290 295 300
- Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu 305 310 315
- Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn 325 330 335
- Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly 340 345 350
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- Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr 370 375 380
- Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala 385 390 395 400
- Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala 405 410 415
- Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln 420 425 430
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- Ser Ala Gly Val Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg
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